AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 9, lines 8-11, with the following paragraph:

Figure 3. The aligned amino acid sequence of the LjNFR5 and PsSYM10 proteins. ~~Amino acid residues sharing identity are highlighted.~~ The *Medicago truncatula* (Ac126779) showing 76 % amino acid ~~identy~~identity to *Lotus* NFR5 is included to exemplify a substantial identical protein sequence.

Please replace the third paragraph on page 17, lines 20-24:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.,* 2002, Nucleic Acids Res. 30: 276-80; and searchable on the internet at ~~http://www.~~ sanger.ac.uk/Software/Pfam[[/]] and on NCBI at ~~http://www.~~ ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi.

with the following paragraph:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.,* 2002, Nucleic Acids Res. 30: 276-80; and searchable on the internet at sanger.ac.uk/Software/Pfam and on NCBI at ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi.

Please replace the fourth paragraph on page 17, lines 26-30:

Protein domain prediction: sequences are analyzed by BLAST (~~www.~~ (ncbi.nlm.nih.gov/BLAST[[/]]) and PredictProtein (~~www.~~ (emblheidelberg.de/predictprotein/predictprotein). Signal peptides are predicted by

SignalP v. 1.1 ~~(www.~~ (cbs.dtu.dk/services/signal[[/]]) and transmembrane regions are predicted by TMHMM v. 2.0 ~~(www.~~ (cbs.dtu.dk/services/TMHMM[[/]]).

with the following paragraph:

Protein domain prediction: sequences are analyzed by BLAST (ncbi.nlm.nih.gov/BLAST) and PredictProtein (emblheidelberg.de/predictprotein/predictprotein). Signal peptides are predicted by SignalP v. 1.1 (cbs.dtu.dk/services/signalP) and transmembrane regions are predicted by TMHMM v. 2.0 (cbs.dtu.dk/services/TMHMM).

Please replace the paragraph on page 19, lines 19-31 through page 20, lines 1-4:

Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: ~~(www~~ ncbi.nlm.nih.gov[[/)]].

with the following paragraph:

Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: ncbi.nlm.nih.gov.

Please replace the paragraph on page 53, lines 17-22, with the following:

Molecular markers based on DNA polymorphism are used to detect the alleles in breeding populations. Similar use can be taken of the *NFR1* sequences. Molecular DNA markers, based on the *NFR5* allele sequence differences of *Lotus* and pea, are bolded in Table 12 and highlighted in ~~Tables 12 and~~Table 13 as examples of how DNA polymorphism can be used directly to detect the presence of an advantageous allele in a breeding population.

Please replace Table 1 on page 55 with the following:

Table 1

Alignment of *Lotus*, *Glycine* and *Phaseolus* NFR5 protein sequences

	1	2	3	4	50
Lotus	MAVFF--	GSLSLFLALT	LLFTNIAARS	EKISGPDFSC	PVDSPPSCET
Glycine	MAVFFPFLPL	HSQILCLVIM	LFSTNIVAQS	QQDNRTNFSC	PSDSPPSCET
Phaseolus	MAVFFVSLTL	GAQILYVVLM	FFTC-	QQTNGTNFSC	PSNSPPSCET
	6	7	8	9	100
Lotus	YVTYTAQSPN	LLSLTNISD	FDISPLSIA	ASNIDAGKDK	LVPGQVLLVP
Glycine	YVTYIAQSPN	FLSLTNISN	FDTSPLSIAR	ASNLEPMDDK	LVKDQVLLVP
Phaseolus	YVTYISQSPN	FLSLTSVSN	FDTSPLSIAR	ASNLQHEEDK	LIPGQVLLI
	11	12	13	14	150
Lotus	VTCGCAGNHS	SANTSYQIQL	GDSYDFVATT	LYENLTNWNI	VQASNPGVNP
Glycine	VTCGCTGNRS	FANISYEINQ	GDSFYFVATT	SYENLTNWRA	VMDLNPVLSP
Phaseolus	VTCGCTGNRS	FANISYEINQ	GDSFYFVATT	LYQNLTNWHA	VMDLNPGLSQ
	16	17	18	19	200
Lotus	YLLPERVKVV	FPLFCRCPSK	NQLNKGIQYL	ITYVWKPNDN	VSLVSAKFGA
Glycine	NKLPIGIQVV	FPLFCKCPSK	NQLDKEIKYL	ITYVWKPGDN	VSLVSDKFGA
Phaseolus	FTLPIGIQV	IPLFCKCPSK	NQLDRGIKYL	ITHVWQPNDN	VSFVSNKLGA
	21	22	23	24	250
Lotus	SPADILTENR	YGQDFTAATN	LPILIPVTQ	PELTQPSSNG	RKSSIHLLV
Glycine	SPEDIMSENN	YGQNFTAANN	LPVLIPVTR	PVLARSPSDG	RKGGIRLPVI
Phaseolus	SPQDILSENN	YGQNFTAASN	LPVLIPVTL	PDLIQSPSDG	RKHRIGLPVI
	26	27	28	29	300
Lotus	LGITLGCTL	TAVLTGTLVY	VYCRRKKALN	RTASSAETAD	KLLSGVSGYV
Glycine	IGISLGCTL	VLVLAVLLVY	VYCLKMKTLN	RSASSAETAD	KLLSGVSGYV
Phaseolus	IGISLGCTL	VVVSAILLVC	VCCLKMKSLN	RSASSAETAD	KLLSGVSGYV
	31	32	33	34	350
Lotus	SKPNVYEIDE	IMEATKDFSD	ECKVGESVYK	ANIEGRVVAV	KKIKEGGANE
Glycine	SKPTMYETDA	IMEATMNLSE	QCKIGESVYK	ANIEGKVLAV	KRFKED-VTE
Phaseolus	SKPTMYETGA	ILEATMNLSE	QCKIGESVYK	ANIEGKVLAV	KRFKED-VTE
	36	37	38	39	400
Lotus	ELKILQKVNH	GNLVKLMGVS	SGYDGNCFLV	YEYAENGSLA	EWLFSKS--
Glycine	ELKILQKVNH	GNLVKLMGVS	SDNDGNCFVV	YEYAENGSLD	EWLFSKSCSD
Phaseolus	ELKILQKVNH	GNLVKLMGVS	SDNDGNCFVV	YEYAENGSLE	EWLFAKSCSE
	41	42	43	44	450
Lotus	-SGTPNSLTW	SQRISIAVDV	AVGLQYMHEH	TYPRIIHRD	TTSNILLDSN
Glycine	TSNSRASLTW	CQRISMAVDV	AMGLQYMHEH	AYPRIVHRDI	TSSNILLDSN
Phaseolus	TSNSRTSLTW	CQRISIAVDV	SMGLQYMHEH	AYPRIVHRDI	TSSNILLDSN
	46	47	48	49	500
Lotus	FKAKIANFAM	ARTSTNPMMP	KIDVFAFGVL	LIELLTGRKA	MTTKENGEVV
Glycine	FKAKIANFSM	ARTFTNPMMP	KIDVFAFGVV	LIELLTGRKA	MTTKENGEVV
Phaseolus	FKAKIANFSM	ARTFTNPMMS	KIDVFAFGVV	LIELLTGRKA	MTTKENGEVV

	51	52	53	54	550	
Lotus	MLWKDMWEIF	DIEENREERI	RKWMDPNLES	FYHIDNALSL	ASLAVNCTAD	
Glycine	MLWKDIWKIF	DQEENREERL	KKWMDPKLES	YYPIDYALSL	ASLAVNCTAD	
Phaseolus	MLWKDIWKIF	DQEENREERL	RKWMDPKLDN	YYPIDYALSL	ASLAVNCTAD	
	56	57	58	59	600	
Lotus	KSLSRPSMAE	IVLSLSFLT	QSSNPTLERS	LTSSGLDVED	DAHIVTSIT	
Glycine	KSLSRPTIAE	IVLSLSLLT	PSP-ATLERS	LTSSGLDVEA	-	
Phaseolus	KSLSRPTIAE	IVLSLSLLT	PSP-ATLERS	LTSSGLDVEA	-	
	61	62	63	65	650	
Lotus	R....	....	....	....	....	SEQ ID NO: 8
Glycine	R....	....	....	....	....	SEQ ID NO: 48
Phaseolus	R....	....	....	....	....	SEQ ID NO: 40

Please replace Table 3 on page 57 with the following:

Table 3

Alignment of *Lotus* and *Pisum* NFR1 protein sequences

	1	2	3	4	50
Pisum	MKLKNGLLLF	F-	KVESKCVIGC	DIALASYYVM	P-
Pisum	MKLKNGLLLF	F-	KVDSKCVKGC	DLALASYYVM	P-
Lotus	MKLKTGLLLF	FILLLGHVC	HVESNCLKGC	DLALASYYI	PGVFILQNI
	6	7	8	9	100
Pisum	TFMQSKLVTN	SFEVIVRYNR	DIVFSNDNLF	SYFRVNIPFP	CECIGGEFLG
Pisum	NYMQSKIVTN	SSDVLNSYNK	VLVTNHGNIF	SYFRINIPF	CECIGGEFLG
Lotus	TFMQSEIVSS	N-	DKILNDINI	SFQRLNIPFP	CDCIGGEFLG
	11	12	13	14	150
Pisum	HVFEYTANEG	DTYDLIANTY	YASLTTVEVL	KKYNSYDPNH	IPVKAKVNVT
Pisum	HVFEYTTKKG	DTYDLIANNY	YVSLTSVELL	KKFNSYDPNH	IPAKAKVNVT
Lotus	HVFEYSASKG	DTYETIANL	YANLTTVDLL	KRFNSYDPKN	IPVNAKVNVT
	16	17	18	19	200
Pisum	VNCSCGNSQI	SKDYGLFITY	PLRPRDTLEK	IARHSNLDEG	VIQSYNLGVN
Pisum	VNCSCGNSQI	SKDYGLFVTY	PLRSTDSLEK	IANESKLDEG	LIQNFNPDVN
Lotus	VNCSCGNSQV	SKDYGLFITY	PIRPGDTLQD	IANQSSLDAG	LIQSFNPSVN
	21	22	23	24	250
Pisum	FSKGSGVVFF	PGRDKNGEYV	PLYPRT-GLG	KGAAAGISI	GIFALLLF
Pisum	FSRGSGIVF	PGRDKNGEYV	PLYPKT-GVG	KGVAIGISI	GVFAVLLFV
Lotus	FSKDSGIAF	PGRYKNGVYV	PLYHRTAGLA	SGAAVGISI	GTFVLLLLA
	26	27	28	29	300
Pisum	CIYIKYFQK	EEEKTKLP-Q	VSTALSAQD-	-ASGSGEYET	SGSSGHGTGS
Pisum	CIYVKYFQKK	EEEKTILP-	VSKALSTQDG	NASSSGEYET	SGSSGHGTGS
Lotus	CMYVRY-QKK	EEEKAKLPTD	ISMALSTQD	-ASSSAEYET	SGSSGPGTAS
	31	32	33	34	350
Pisum	TAGLTGIMVA	KSTEFSYQEL	AKATNNFSLD	NKIGQGGFGA	VYYAVLRGEK

Pisum	AAGLTGIMVA	KSTEFSYQEL	AKATDNFSLD	NKIGQGGFGA	VYYAELRGEK
Lotus	ATGLTSIMVA	KSMEFSYQEL	AKATNNFSLD	NKIGQGGFGA	VYYAELRGKK
	36	37	38	39	400
Pisum	TAIKKMDVQA	STEFLCELQV	LTHVHHLNLV	RLIGYCVEGS	LFLVYEHID
Pisum	TAIKKMNVQA	SSEFLCELKV	LTHVHHLNLV	RLIGYCVEGS	LFLVYEHID
Lotus	TAIKKMDVQA	STEFLCELKV	LTHVHHLNLV	RLIGYCVEGS	LFLVYEHID
	41	42	43	44	450
Pisum	GNLGQYLHGI	DKAPLPWSSR	VQIALDSARG	LEYIHEHTVP	VYIHRDVKSA
Pisum	GNLGQYLHGK	DKEPLPWSSR	VQIALDSARG	LEYIHEHTVP	VYIHRDVKSA
Lotus	GNLGQYLHGS	GKEPLPWSSR	VQIALDAARG	LEYIHEHTVP	VYIHRDVKSA
	46	47	48	49	500
Pisum	NILIDKNLH	KVADFGLTKL	IEVGNSTLHT	RLVGTFGYMP	PEYAQYGDVS
Pisum	NILIDKNLR	KVADFGLTKL	IEVGNSTLHT	RLVGTFGYMP	PEYAQYGDVS
Lotus	NILIDKNLR	KVADFGLTKL	IEVGNSTLQT	RLVGTFGYMP	PEYAQYGDIS
	51	52	53	54	550
Pisum	PKIDVYAFGV	VLYELISAK	AILKTGESAV	-	EEALNQIDPL
Pisum	PKIDVYAFGV	VLYELISAK	AVLKTGEESV	AESKGLVALF	EKALNQIDPS
Lotus	PKIDVYAFGV	VLFELISAK	AVLKTGE-	AESKGLVALF	EEALNKSDPC
	56	57	58	59	600
Pisum	EALRKLVDPR	LKENYPIDSV	LKMAQLGRAC	TRDNPLLRPS	MRSLVVALMT
Pisum	EALRKLVDPR	LKENYPIDSV	LKMAQLGRAC	TRDNPLLRPS	MRSLVVDLMT
Lotus	DALRKLVDPR	LGENYPIDSV	LKIAQLGRAC	TRDNPLLRPS	MRSLVVALMT
	61	62	63	65	650
Pisum	LLSHTDD--	DTFYENQSLT	NLLSVR..	....	SEQ ID NO: 52
Pisum	LSSPFEDCDD	DTSYENQTLI	NLLSVR..	....	SEQ ID NO: 54
Lotus	LSSLTEDCDD	ESSYESQTLI	NLLSVR..	....	SEQ ID NO: 24

Please replace Table 12 on page 65 with the following:

Table 12

Nucleotide sequence variation between the pea *SYM10* alleles of pea cultivars Frisson and Finale*

```
Frisson    CTTGCATTTC TTCACAATTT CACAACAATG GCTATCTTCT TTCTTCCTTC
Finale     CTTGCATTTC TTCACAATTT CACAACAATG GCTATCTTCT TTCTTCCTTC

Frisson    TAGTTCTCAT GCCCTTTTTC TTGCACTCAT GTTTTTTGTC ACTAATATTT
Finale     TAGTTCTCAT GCCCTTTTTC TTGCACTCAT GTTTTTTGTC ACTAATATTT

Frisson    CAGCTCAACC ATTACAACTC AGTGGAACAA ACTTTTCATG CCCGGTGGAT
Finale     CAGCTCAACC ATTACAACTC AGTGGAACAA ACTTTTCATG CCCGGTGGAT

Frisson    TCACCTCCTT CATGTGAAAC CTATGTGACA TACTTTGCTC GGTCTCCAAA
Finale     TCACCTCCTT CATGTGAAAC CTATGTGACA TACTTTGCTC GGTCTCCAAA

Frisson    CTTTTTGAGC CTAACTAACA TATCAGATAT ATTTGATATG AGTCCTTTAT
Finale     CTTTTTGAGC CTAACTAACA TATCAGATAT ATTTGATATG AGTCCTTTAT

Frisson    CCATTGCAAA AGCCAGTAAC ATAGAAGATG AGGACAAGAA GCTGGTTGAA
Finale     CCATTGCAAA AGCCAGTAAC ATAGAAGATG AGGACAAGAA GCTGGTTGAA

Frisson    GGCCAAGTCT TACTCATACC TGTAACTTGT GGTTGCACTA GAAATCGCTA
Finale     GGCCAAGTCT TACTCATACC TGTAACTTGT GGTTGCACTA GAAATCGCTA

Frisson    TTTCGCGAAT TTCACGTACA CAATCAAGCT AGGTGACAAC TATTTCATAG
Finale     TTTCGCGAAT TTCACGTACA CAATCAAGCT AGGTGACAAC TATTTCATAG

Frisson    TTTCAACCAC TTCATACCAG AATCTTACAA ATTATGTGGA AATGGAAAAT
Finale     TTTCAACCAC TTCATACCAG AATCTTACAA ATTATGTGGA AATGGAAAAT

Frisson    TTCAACCCTA ATCTAAGTCC AAATCTATTG CCACCAGAAA TCAAAGTTGT
Finale     TTCAACCCTA ATCTAAGTCC AAATCTATTG CCACCAGAAA TCAAAGTTGT

Frisson    TGTCCCTTTA TTCTGCAAAT GCCCCTCGAA GAATCAGTTG AGCAAAGGAA
Finale     TGTCCCTTTA TTCTGCAAAT GCCCCTCGAA GAATCAGTTG AGCAAAGGAA

Frisson    TAAAGCATCT GATTACTTAT GTGTGGCAGG CTAATGACAA TGTTACCCGT
Finale     TAAAGCATCT GATTACTTAT GTGTGGCAGG CTAATGACAA TGTTACCCGT

Frisson    GTAAGTTCCA AGTTTGGTGC ATCACAAGTG GATATGTTTA CTGAAAACAA
Finale     GTAAGTTCCA AGTTTGGTGC ATCACAAGTG GATATGTTTA CTGAAAACAA

Frisson    TCAAAACTTC ACTGCTTCAA CCAACGTTCC GATTTTGATC CCTGTGACAA
Finale     TCAAAACTTC ACTGCTTCAA CCAATGTTCC GATTTTGATC CCTGTGACAA
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Frisson    AGTTACCGGT AATTGATCAA CCATCTTCAA ATGGAAGAAA AAACAGCACT
Finale     AGTTACCGGT AATTGATCAA CCATCTTCAA ATGGAAGAAA AAACAGCACT

Frisson    CAAAAACCTG CTTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT
Finale     CAAAAACCTG CTTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT

Frisson    TGTAGTTTTA ACACTATCAC TTGTTTATGT ATATTGTCTG AAAATGAAGA
Finale     TGTAGTTTTA ACACTATCAC TTGTTTATGT ATATTGTCTG AAAATGAAGA

Frisson    GATTGAATAG GAGTACTTCA TTGGCGGAGA CTGCGGATAA GTTACTTTCA
Finale     GATTGAATAG GAGTACTTCA TTGGCGGAGA CTGCGGATAA GTTACTTTCA

Frisson    GGTGTTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT
Finale     GGTGTTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT

Frisson    CATGGAAGCT ACAATGAACC TGAGTGAGAA TTGTAAGATT GGTGAATCCG
Finale     CATGGAAGCT ACAATGAACC TGAGTGAGAA TTGTAAGATT GGTGAATCTG

Frisson    TTTACAAGGC TAATATAGAT GGTAGAGTTT TAGCAGTGAA AAAAATCAAG
Finale     TTTACAAGGC TAATATAGAT GGTAGAGTTT TAGCAGTGAA AAAAATCAAG

Frisson    AAAGATGCTT CTGAGGAGCT GAAAATTTTG CAGAAGGTAA ATCATGGAAA
Finale     AAAGATGCTT CTGAGGAGCT GAAAATTCTG CAGAAGGTAA ATCATGGAAA

Frisson    TCTTGTGAAA CTTATGGGTG TGTCTTCCGA CAACGACGGA AACTGTTTCC
Finale     TCTTGTGAAA CTTATGGGTG TGTCTTCCGA CAACGAAGGA AACTGTTTCC

Frisson    TTGTTTACGA GTATGCTGAA AATGGATCAC TTGATGAGTG GTTGTTCTCA
Finale     TTGTTTACGA GTATGCTGAA AATGGATCAC TTGATGAGTG GTTGTTCTCA

Frisson    GAGTCGTCGA AAACTTCGAA CTCGGTGGTC TCGCTTACAT GGTCTCAGAG
Finale     GAGTTGTCGA AAACTTCGAA CTCGGTGGTC TCGCTTACAT GGTCTCAGAG

Frisson    AATAACAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC
Finale     AATAACAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC

Frisson    ATACTTACCC AAGAATAATC CACAGAGACA TCACAACAAG TAATATCCTT
Finale     ATACTTACCC AAGAATAATC CACAGAGACA TCACAACAAG TAATATCCTT

Frisson    CTGGATTCAA ACTTTAAGGC CAAGATAGCG AATTTTTCAA TGGCCAGAAC
Finale     CTGGATTCAA ACTTTAAGGC CAAGATAGCG AATTTTTCAA TGGCCAGAAC

Frisson    TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG
Finale     TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG

Frisson    TTCTGATTGA GTTGCTTACC GGCAAGAAAG CGATAACAAC GATGGAAAAT
Finale     TTCTGATTGA GTTGCTTACC GGCAAGAAAG CGATAACAAC GATGGAAAAT

Frisson    GGCGAGGTGG TTATTCTGTG GAAGGATTTC TGGAAGATTT TTGATCTAGA
Finale     GGCGAGGTGG TTATTCTGTG GAAGGATTTC TGGAAGATTT TTGATCTAGA
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Frisson    AGGGAATAGA GAAGAGAGCT TAAGAAAATG GATGGATCCT AAGCTAGAGA
Finale     AGGGAATAGA GAAGAGAGCT TAAGAAAATG GATGGATCCT AAGCTAGAGA

Frisson    ATTTTTATCC TATTGATAAT GCTCTTAGTT TGGCTTCTTT GGCAGTGAAT
Finale     ATTTTTATCC TATTGATAAT GCTCTTAGTT TGGCTTCTTT GGCAGTGAAT

Frisson    TGTACTGCAG ATAAATCATT GTCAAGACCA AGCATTGCAG AAATTGTTCT
Finale     TGTACTGCAG ATAAATCATT GTCAAGACCA AGCATTGCAG AAATTGTTCT

Frisson    TTGTCTTTCT CTTCTCAATC AATCATCATC TGAACCAATG TTAGAAAGAT
Finale     TTGTCTTTCT CTTCTCAATC AATCATCATC TGAACCAATG TTAGAAAGAT


Frisson    CCTTGACATC TGGTTTAGAT GTTGAAGCTA CTCATGTTGT TACTTCTATA
Finale     CCTTGACATC TGGTTTAGAT GTTGAAGCTA CTCATGTTGT TACTTCTATA

Frisson    GTAGCTCGTT GATATTCATT CAAGTGAAGG TAACACTGAA TCAATGCTTC
Finale     GTAGCTCGTT GATATTCATT CAAGTGAAGG TAACACTAAA TCAATGCTTC

Frisson    AGTTTCTTAT ATTCAAGATG GTTACTTTGT TTAGATGATT ATTGATTACA
Finale     AGTTTCTTAT ATTCAAGATG GTTACTTTGT TTAGGTGATT ATTGATTACA

Frisson    TCTTTATGTG TGGAACTATA TGGTTATTTT AATTAAGGGA ATTGTTCTAA
Finale     TCTTTATGTG TGGAACTATA TGGTTATTTT AATTAAGGGA ATTAGTCTAA

Frisson    AATTCATTTT TCCATGTT   SEQ ID NO: 13
Finale     ATTTCATTTT TCCATGTT   SEQ ID NO: 12
```

* Nucleotide differences are bolded and the coding region is underlined